

nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearoyl ACP desaturase, or the complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (iv) (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn stearic acid phenotype.

173. (twice amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid

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sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, and (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or (2) the isolated nucleic acid fragment of (ii) (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, and (b) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or

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(2) the isolated nucleic acid fragment of (iv) (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; wherein expression of the chimeric gene results in an altered corn oleic acid phenotype.

174. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises a chimeric gene selected from the group consisting of:

(i) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, and a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 stearyl ACP desaturase, or the complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(ii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, and (c)

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an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (ii) (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences,

(iii) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(iv) a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or the complement thereof, (b) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or the complement thereof, (c) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (2) the isolated nucleic acid fragment of (iv)(b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, and (d) a shrunken 1

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intron/exon, operably linked to suitable regulatory sequences, wherein expression of the chimeric gene results in an altered corn oil phenotype.

175. (twice amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of a corn grain obtained from a corn plant or plant part which comprises a chimeric gene comprising (a) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1, 58 or 59, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, (b) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (1) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or (2) the isolated nucleic acid fragment of (b) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences, and (c) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences;

wherein expression of the chimeric gene results in an altered corn oleic acid phenotype, and

further wherein the corn grain has an oil content in the range from about 6% to about 10% on a dry matter basis and further wherein said oil is comprised of not less than 60% oleic acid of the total oil content of the seed.

176. (once amended) A method of improving the carcass quality of an animal by feeding the animal a carcass quality improving amount of animal feed derived from the processing of corn grain obtained from a corn plant or plant part which comprises

(i) a first chimeric gene selected from the group consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS: 9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

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(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment of (b) (2) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase wherein said desaturase has an amino acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a second polypeptide selected from SEQ ID NOS:9 or 11, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-9 stearyl ACP desaturase, or the complement of either the fragment or subfragment, (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS:19 or 38-49 or (B) the isolated nucleic acid fragment of (d)(2) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory

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sequences, and (3) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences, and

(ii) a second chimeric gene selected from the set consisting of:

(a) a chimeric gene comprising an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, operably linked to suitable regulatory sequences;

(b) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, and (2) an isolated nucleic acid fragment comprising a corn oleosin promoter wherein said promoter can be full length or partial and said promoter: (A) comprises a nucleotide sequence having a sequence identity of at least 80% based on the Clustal method of alignment when compared to the nucleotide sequence in any of SEQ ID NOS: 19 or 38-49 or (B) the isolated nucleic acid fragment of (b) (2) hybridizes to the nucleotide sequence set forth in SEQ ID NOS: 19 or 38-49 under moderately stringent conditions, operably linked to suitable regulatory sequences;

(c) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 desaturase, or the complement of either the fragment or subfragment, and (2) a shrunken 1 intron/exon, operably linked to suitable regulatory sequences; or

(d) a chimeric gene comprising (1) an isolated nucleic acid fragment encoding a corn delta-12 desaturase wherein said fragment has a nucleic acid sequence identity of at least 80% based on the Clustal method of alignment when compared to a nucleic acid as set forth in SEQ ID NOS: 1 or 2, or a functionally equivalent subfragment of the isolated nucleic acid fragment encoding a corn delta-12 stearyl ACP desaturase, or the complement of

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